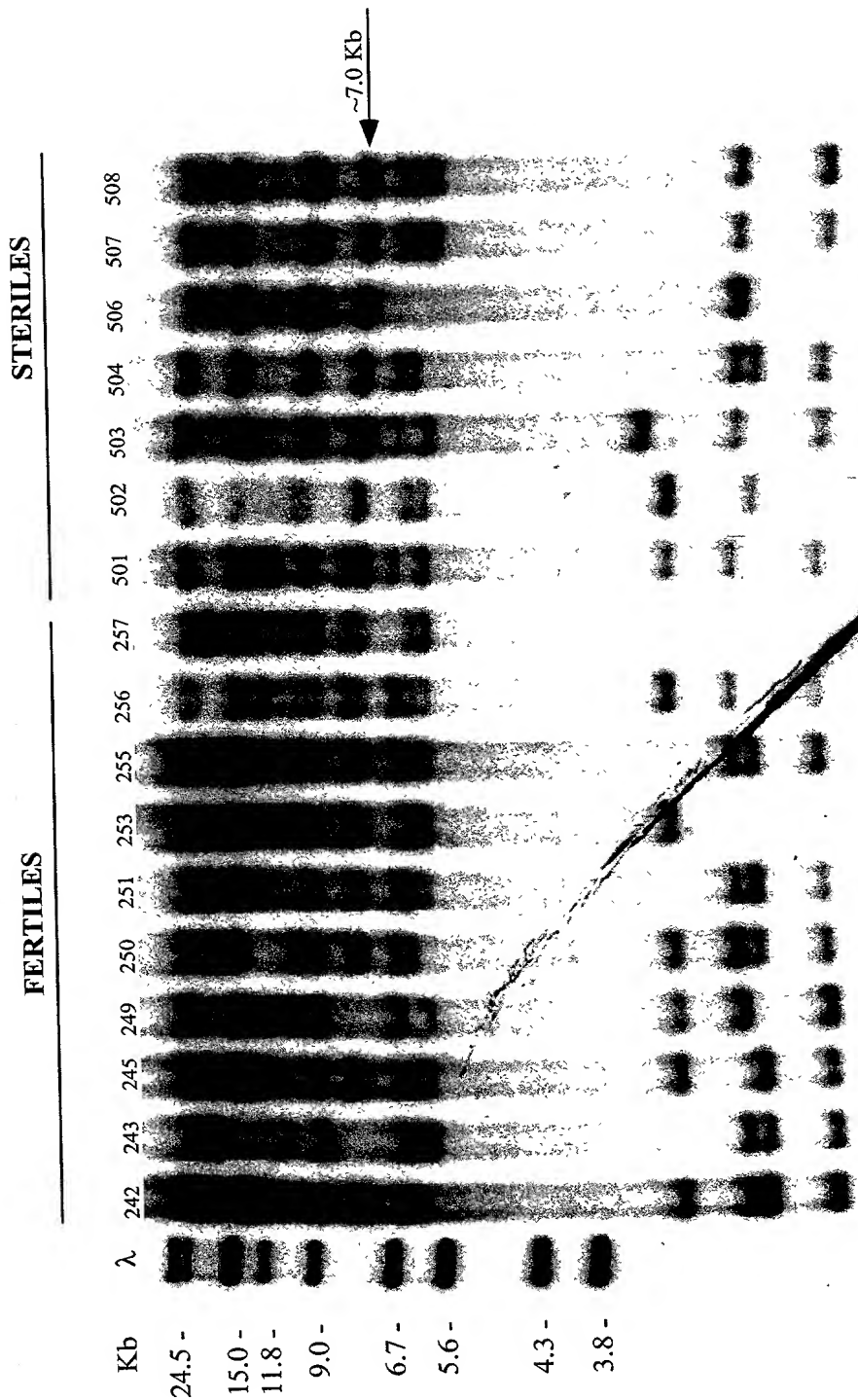


FIGURE 1



SOUTHERN OF ECORI DIGESTED DNA FROM THE MALE STERILE FAMILY BS92-7. HYBRIDIZED WITH THE MU1 TRANSPOSON.

Figure 2

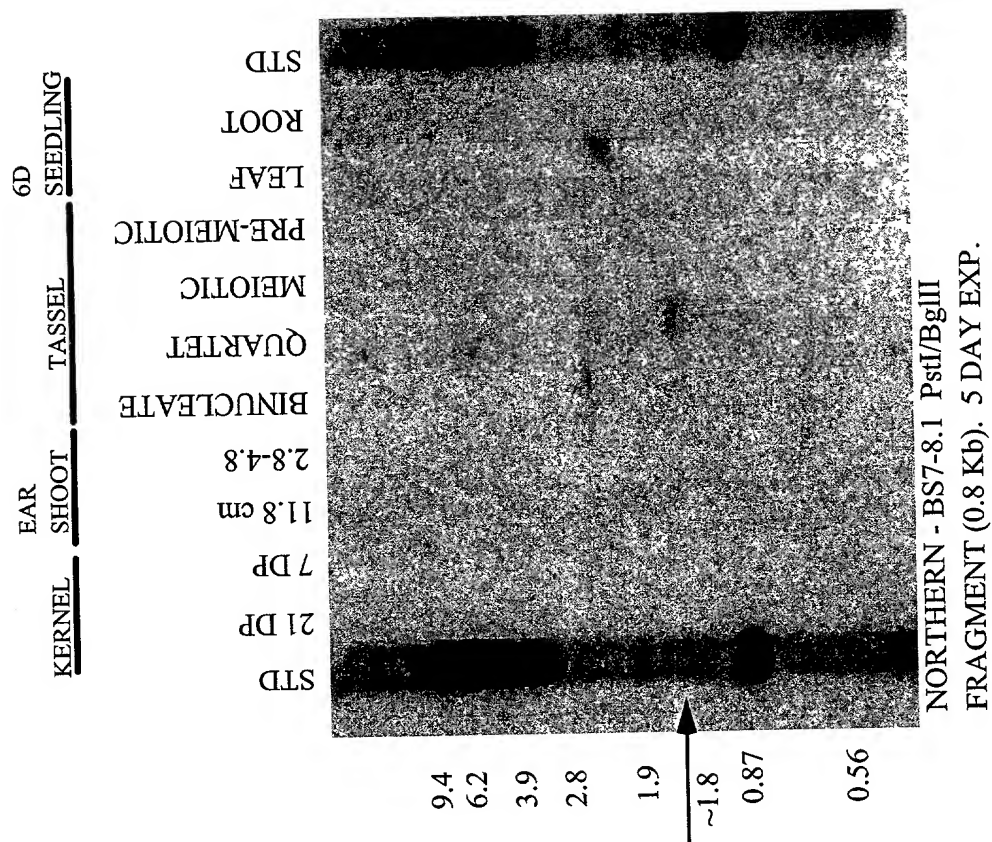


FIGURE 3

FIGURE 4

GGTGACCTCAAGCAAGGGCAAGGTATGCGTAACCGGGGCCTCAGGCTTTGTTGCCTCTTG
1 -----+-----+-----+-----+-----+-----+-----+ 60
CCACTGGAGTTCGTTCCCGTTCCATACGCATTGGCCCCGGAGTCCGAAACAACGGAGAAC

b V T S S K G K V C V T G A S G F V A S W -

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GCTTATCAAACGGCTCCTCGAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCCAGG
61 -----+-----+-----+-----+-----+-----+ 120
CGAATAGTTTGGCGAGGAGCTCAGACCTATAGTACACCATCCCTGACAGTCCCTGGGTCC

b L I K R L L E S G Y H V V G T V R D P G -

AAATCACCAAAAAACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT
121 -----+-----+-----+-----+-----+-----+ 180
TTTAGTGGTTTTTTTGTGGGTGGAACCTTTAATGGACCGGATTCTCTCCGACGTTTA

b N H Q K T A H L W K L P G A K E R L Q I -

CGTGCGAGCTAATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGGCCTGTGAGGG
181 -----+-----+-----+-----+-----+-----+ 240
GCACGCTCGATTAGACAACCTTCTTCCCTCGAAGCTGTCGCGGCACTACCGGACACTCCC

b V R A N L L E E G S F D S A V M A C E G -

TGTATTCCACACTGCATCCCCCGTCCTCGCTAAACCCGACTCTACTAGCAAGGAGGACAC
241 -----+-----+-----+-----+-----+-----+ 300
ACATAAGGTGTGACGTAGGGGGCAGGAGCGATTGGGCTGAGATGATCGTTCCTCCTGTG

b V F H T A S P V L A K P D S T S K E D T -

GCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGATCGTGCAAGAAGAACCCTT
301 -----+-----+-----+-----+-----+-----+ 360
CGAGCAGGGACGCCACTTGCCATGAGACTTGACGACTCTAGCACGTTCTTCTTGGGGAA

b L V P A V N G T L N V L R S C K K N P F -

CCTGAAAAGGGTCGTCCTTACGTCTTCGTGCTGCGGTGAGGATCAGGGACGACGGTGG
361 -----+-----+-----+-----+-----+-----+ 420
GGACTTTTCCCAGCAGGAATGCAGAAGCAGCAGACGCCACTCCTAGTCCCTGCTGCCACC

b L K R V V L T S S S S A V R I R D D G G -

CCAGTCCAGTAACATCTCGCTGGACGAAACGACATGGAGCTCCGTGCCACTCTGCGAGAA
421 -----+-----+-----+-----+-----+-----+ 480
GGTCAGGTCATTGTAGAGCGACCTGCTTTGCTGTACCTCGAGGCACGGTGAGACGCTCTT

b Q S S N I S L D E T T W S S V P L C E K -

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FIGURE 4B

GATGCATCTATGGTATGCCCTAGCCAAGGTATTTGCAGAGAAAGCGGCGTGGGAGTTTCGC
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 CTACGTAGATAACCATACGGGATCGGTTCCATAAACGTCTCTTTGCGCCGACCCCTCAAGCG
 b M H L W Y A L A K V F A E K A A W E F A -
 CAAGGAGAACGGCATCGACCTTGTGACTGTCCTCCCGTCGTTTCGTGATCGGGCCCAGTTT
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 GTTCCTCTTGCCGTAGCTGGAACACTGACAGGAGGGCAGCAAGCACTAGCCCCGGGTCAAA
 b K E N G I D L V T V L P S F V I G P S L -
 GTCCACGAGCTATGCGTTACCGCTTCAGACGTCCTAGGCCTATTCCAAGGCGACACGGC
 601 -----+-----+-----+-----+-----+-----+-----+ 660
 CAGGGTGCTCGATACGCAATGGCGAAGTCTGCAGGATCCGGATAAGGTTCCGCTGTGCCG
 b S H E L C V T A S D V L G L F Q G D T A -
 AAGGTTTCAGCTCGTACGGAAGAATGGGGTACGTCCACATCGACGACGTTGCGAGCAGCCA
 661 -----+-----+-----+-----+-----+-----+-----+ 720
 TTCCAAGTCGAGCATGCCTTCTTACCCCATGCAGGTGTAGCTGCTGCAACGCTCGTCGGT
 b R F S S Y G R M G Y V H I D D V A S S H -
 CATCCTGGTGTACGAGGTCCCCAGGCCGCGGGAGGTACCTGTGCAGCTCAGTGGTGCT
 721 -----+-----+-----+-----+-----+-----+-----+ 780
 GTAGGACCACATGCTCCAGGGGTCCGGCGGCCCTCCATGGACACGTCGAGTCACCACGA
 b I L V Y E V P Q A A G R Y L C S S V V L -
 GGACAACGACGAGCTGGTCTCCTCGCTCGCGAAACGCTACCCGATATTCCCCATACCCCG
 781 -----+-----+-----+-----+-----+-----+-----+ 840
 CCTGTTGCTGCTCGACCAGAGGAGCGAGCGCTTTGCGATGGGCTATAAGGGGTATGGGGC
 b D N D E L V S S L A K R Y P I F P I P R -
 GAGGCTGAACAGCCCCTACGGCAAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGG
 841 -----+-----+-----+-----+-----+-----+-----+ 900
 CTCCGACTTGTCGGGGATGCCGTTTCGTACGATGGTTCGACTTGTGCAGCTTCGACGTCCC
 b R L N S P Y G K Q S Y Q L N T S K L Q G -
 GCTGGGCTTCAAGTTTCAGAGGGGTGCAGGAGATGTTTCGACGACTGCGTGCAGTCGCTCAA
 901 -----+-----+-----+-----+-----+-----+-----+ 960
 CGACCCGAAGTTCAAGTCTCCCCACGTCCTCTACAAGCTGCTGACGCACGTACGCGAGTT
 b L G F K F R G V Q E M F D D C V Q S L K -
 AGACCAGGGCCACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGGGGTGCCTCCTGTGAA
 961 -----+-----+-----+-----+-----+-----+-----+ 1020
 TCTGGTCCCGGTGGACGACCTACGGGGGACACTTGACGCTACCCCCACGGAGGACACTT
 b D Q G H L L E C P L *

FIGURE 4C

CGCCCGTTTTTTTTTTCTTCAATAATTCCACGTCATGTCACGGTGTCTCGCGCAGACT
 1021 -----+-----+-----+-----+-----+-----+ 1080
 GCGGGCAAAAAAAAAAAGAAGTTATTAAGGTGCAGTACAGTGCCACAGGAGCGCGTCTGA

GCTACTGTCAGGTGTCAGGGCGTCATAGCTCACGGGCTCTACGGCTACATGAATAAAATG
 1081 -----+-----+-----+-----+-----+-----+ 1140
 CGATGACAGTCCACAGTCCCGCAGTATCGAGTGCCCGAGATGCCGATGTACTTATTTTAC

TCACGCTAGCTCGTCATTTGCTTTGCCATTTAAAAAAAAAAAAAAAAAAAAAACTCGAG
 1141 -----+-----+-----+-----+-----+-----+ 1197
 AGTGCGATCGAGCAGTAAACGAAACGGTAAATTTTTTTTTTTTTTTTTTTTGGAGCTC

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FIGURE 5

1 GAATTCTCGT CTCGGCGGTC AACTGAACCG TAAACAGTGG AAAGTGGATA
 51 CTCTTTCTCT CTCTGCAATC CGTGCCGTGG AAGCAAATGG CGCAGTCGCC
 101 TACTTATCAC ACCAACTTAT CACCTAGAAA AGCGACGCGT CCTGGATCGA
 151 TTGCAAATCT ACCTCCAACC AACCCAGCTT TGTATCTGCT TACTGTGATC
 201 ACCAAAGTTG TGCTGATACG ATGTGCGATT ATTGCTCTTT CTTCTCTAGA
 251 ATGTTCTGTC CGATGCTTTA TAAGAGAAGG TTGGTCAGCA TCGATCTCTG
 301 CCAGTGCTTA GCTGAGAACA TGGTGACCTC AAGCAAGGGC AAGGTATGCG
 351 TAACCGGGGC CTCAGGCTTT GTTGCCCTCTT GGCTTATCAA ACGGCTCCTC
 401 GAGTCTGGAT ATCATGTGGT AGGGACTGTC AGGGACCCAG GTATTTGCGA
 451 AATATCATTA CTATCGTATC AGTCCTCTTT ATTACATTAA TAATTCTTGA
 501 TTACCAATTT TTTCTTTTTT TTTTTTGGTA ACCCACAAGG AAATCACCAA
 551 AAGACAGCCC ACCTTTGGAA ATTACCTGGC GCTAAAGAGA GGCTGCAAAT
 601 CGTGCGAGCT GATCTGTTGG AAGAAGGGAG CTTCGACAGC GCCGTGATGG
 651 CCTGTGAGGG TGTATTCCAC ACTGCATCCC CCGTCCTCGC TAAACCCGAC
 701 TCTACTAGCA AGGCATGCCA TCGCCGATA TATATATGCA TATCTGGACC
 751 ATGCATCCTA CTGCAGCCTT TTCTATACGG AAGCGCGTTG CATCTACCGT
 801 ACGTGAAGCT AGCTATCTAA GCTAAGCTGT TTTTCATGCA TGCATGGTGC
 851 AGGAGGACAC GCTCGTCCCT GCGGTGAACG GTACTCTGAA CGTGCTGAGA
 901 TCGTGCAAGA AGAACCCGTT CCTGAAAAGG GTCGTCTTA CGTCTTCGTC
 951 GTCTGCGGTG AGGATCAGGG ACGACGGTGG CCAGTCCAGT AACATCTCGC
 1001 TGGACGAAAC GACATGGAGC TCCGTGCCAC TCTGCGAGAA GATGCATGTG
 1051 AGATACTACT GAACAGTGTC TACTCTCTCT CTCTCTGTCA TCGATCTCAA
 1101 ACCGTGATCT GAAAAACACG CATGCGCGCA CACGTTGCCG TCGTCGTCCC
 1151 TTTTGTGTGT CACCCGAAGC TATGGTATGC CCTAGCCAAG GTATTTGCAG
 1201 AGAAAGCGGC GTGGGAGTTC GCCAAGGAGA ACGGCATCGA CCTTGTGACT
 1251 GTCCTCCCGT CGTTCGTGAT CGGGCCCAGT TTGTCCCACG AACTATGCGT
 1301 TACCGCTTCA GACGTCCTAG GCCTATTCCA AGGTATTCAT CTCAATCATT

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1351 CGTACGTGTT CTGGTTTTTCG TATGTTAAAT AGATGACTGG AAACAAGAGG
1401 TATACATATA TATACTCTCT GTTCCTCCTC CCCCCCCCCC CCCACCCCCA
1451 GGCGACACGG CAAGGTTTCAG CTCGTACGGA AGAATGGGGT ACGTCCACAT
1501 CGACGACGTT GCGAGCAGCC ACATCCTGGT GTACGAGGCC CCCCAGGCCG
1551 CCGGGAGGTA CCTGTGCAGC TCAGTGGTGC TGGACAACGA CGAGCTGGTC
1601 TCCTCGCTCG CGAAACGCTA CCCGATATTC CCCATACCCC GGAGGTCAGT
1651 CGTCGTCGCG TCGTCTGGAT GTGCGTGCCA TTTTAAGATC TCTGAACGGG
1701 AGAGCCGTGT GCATGGTCCG TTCTGCTGCA GGCTGAACAG CCCCTACGGC
1751 AAGCAGTCGT ACCAGCTGAA CACGTCGAAG CTGCAGGGGC TGGGCTTCAA
1801 GTTCAGAGGG GTGCAGGAgA TGTTCGACgA CTGCGTACAG TCGCTCAAAG
1851 ACCAGGGACA CCTGCTGGAG TGCCCCCTGT GAACTGCGAT GGGGTGCCTC
1901 CGCCTGTGAA CGCGCCGGTT GGGTTGCGTC CCGAACCCGC TGTTAATTGG
1951 TTTTTTTTTTTC TTCAATAATT CCACGTCATG TCACGGTGTC CTCGCGCgA
2001 CTGCTACTGT CAGGGCGTCA TAGCTCACGG GCTCTCCGGC TACATGAATA
2051 AAAATGTCAC GCTCGTCATT TGCTTTGCCT TTTTTTTTGG GTTCGTTCTG
2101 CGAaCTTCCG TTCGCTGTGT GTACTTGTGG CTGCCGGTCg CCTTGTCgGT
2151 GTGGCGACTG ATGATGGTGA TCGGAGGCAG GCACCGGTGT GTGCGTGCGA
2201 TCAACCGAAC GCCATGTGGC GGT TTGGATG GACGAATGGC TCCACCATCG
2251 ATCTGAGTCA TTCGGATTTT GAACCGCTGA TTTGTCCACT GGACGGCACT
2301 AGCATCAAGA TTCAGTCTCA AATCCCAAAT TCCTCAACGC AAAGCCACAA
2351 AGAGAGAATG AATGTACAGT GTTTCAGCC ACAGCTCAcT AGcTCAAAAG
2401 TAGTGAGCAT GcACACCTGT ATTTACATGC ATGCATGTAC ACCCCCACCC
2451 CCACTACTTG TACACTTTGT AAACCAACCA ACCAACCAAC CAAGCAAGCA
2501 ATCAAGCAAA CACACAGAGC AAACCGTACG TGGCTGGCGC C

Figure 6

```

301 CCAGTGTCTAGCTGAGAACATGGTGACCTCAAGCAAGGGCAAGGTATGCG 350
      |||||||||||||||||||||||||||||||||||||||
1  .....GGTGACCTCAAGCAAGGGCAAGGTATGCG 29

351 TAACCGGGGCTCAGGCTTTGTTGCCTCTTGGCTTATCAAACGGCTCCTC 400
      |||||||||||||||||||||||||||||||||||||||
30 TAACCGGGGCTCAGGCTTTGTTGCCTCTTGGCTTATCAAACGGCTCCTC 79

401 GAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCCAGGTATTTGCGA 450
      |||||||||||||||||||||||||||||||||||
80 GAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCC..... 117

      .
      .

501 TTACCAATTTTTCTTTTTTTTTTTTGGTAACCCACAAGGAAATCACCAA 550
      |||||||||||||||
118 .....AGGAAATCACCAA 130

551 AAGACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT 600
      || |||||||||||||||||||||||||||||||||||
131 AAAACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT 180

601 CGTGCGAGCTGATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGG 650
      ||||||||| |||||||||||||||||||||||||||
181 CGTGCGAGCTAATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGG 230

651 CCTGTGAGGCTGTATTCCACACTGCATCCCCCGTCCTCGCTAAACCCGAC 700
      |||||||||||||||||||||||||||||||||||
231 CCTGTGAGGCTGTATTCCACACTGCATCCCCCGTCCTCGCTAAACCCGAC 280

701 TCTACTAGCAAGGCATGCCATCGCCGCATATATATATGCATATCTGGACC 750
      |||||||||
281 TCTACTAGCA..... 290

      .
      .

851 AGGAGGACACGCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGA 900
      |||||||||||||||||||||||||||||||||||
291 AGGAGGACACGCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGA 340

901 TCGTGCAAGAAGAACCCGTTCTGAAAAGGGTCGTCTTACGTCTTCGTC 950
      ||||||||||||| |||||||||||||||||||
341 TCGTGCAAGAAGAACCCCTTCTGAAAAGGGTCGTCTTACGTCTTCGTC 390

951 GTCTGCGGTGAGGATCAGGGACGACGGTGGCCAGTCCAGTAACATCTCGC 1000
      |||||||||||||||||||||||||||||||
391 GTCTGCGGTGAGGATCAGGGACGACGGTGGCCAGTCCAGTAACATCTCGC 440

```

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FIGURE 6C

```

1751 AAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGGGCTGGGCTTCAA 1800
      |||||||||||||||||||||||||||||||||||||||||||||||
863  AAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGGGCTGGGCTTCAA 912

1801 GTTCAGAGGGGTGCAGGAGATGTTTCGACgACTGCGTACAGTCGCTCAAAG 1850
      |||||||||||||||||||||||||||||||||||||||||||||||
913  GTTCAGAGGGGTGCAGGAGATGTTTCGACGACTGCGTGCAGTCGCTCAAAG 962

1851 ACCAGGGACACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGGGTGCCTC 1900
      ||||||| |||||||||||||||||||||||||||||||| |
963  ACCAGGGCCACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGG..GGTGC 1010

1901 CGCCTGTGAACGCGCCGGTTGGGTTGCGTCCCGAACCCGCTGTTAATTCG 1950
      | |||||||||
1011 CTCCTGTGAACGCC...GTT 1028

1951 TTTTTTTTTCTTCAATAATTCCACGTCATGTCACGGTGTCTCGCGCagA 2000
      |||||||||||||||||||||||||||||||||||||||||||
1029 TTTTTTTTTCTTCAATAATTCCACGTCATGTCACGGTGTCTCGCGCAGA 1078

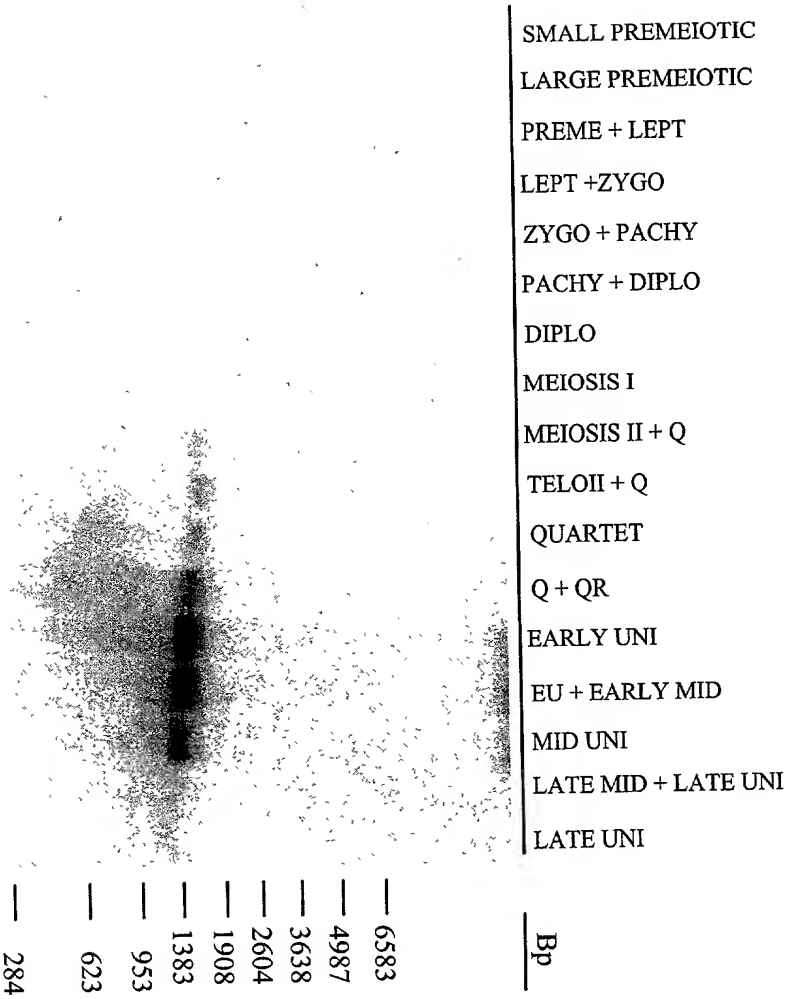
2001 CTGCTAC.....TGTCAGGGCGTCATAGCTCACGGGCTCTCCGGCTAC 2043
      ||||||| |||||||||||||||||||||||||||||
1079 CTGCTACTGTCAGGTGTCAGGGCGTCATAGCTCACGGGCTCTACGGCTAC 1128

2044 ATGAATAAAA...ATGTCACGCTCGTCATTTGCTTTGCCTTTTTTTTTTGG 2090
      ||||||||| | ||||||||||||||||||| |||
1129 ATGAATAAAATGTCACGCTAGCTCGTCATTTGCTTTGCCATTTAAAAAAA 1178

2091 GTTCGTTCTGCGAaCTTCCGTTGCTGTGTGTAATTGTGGCTGCCGGTc 2140
      |
1179 AAAAAAAAAAAAACTCGAG..... 1197

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20050301 013000



DEVELOPMENTAL GENE EXPRESSION IN MICROSPORO-
 GENESIS OF THE MALE FERTILITY GENE BS92-7.
 23 HR. EXP

FIGURE 7

Normalized Luciferase Activity as a % of Wildtype

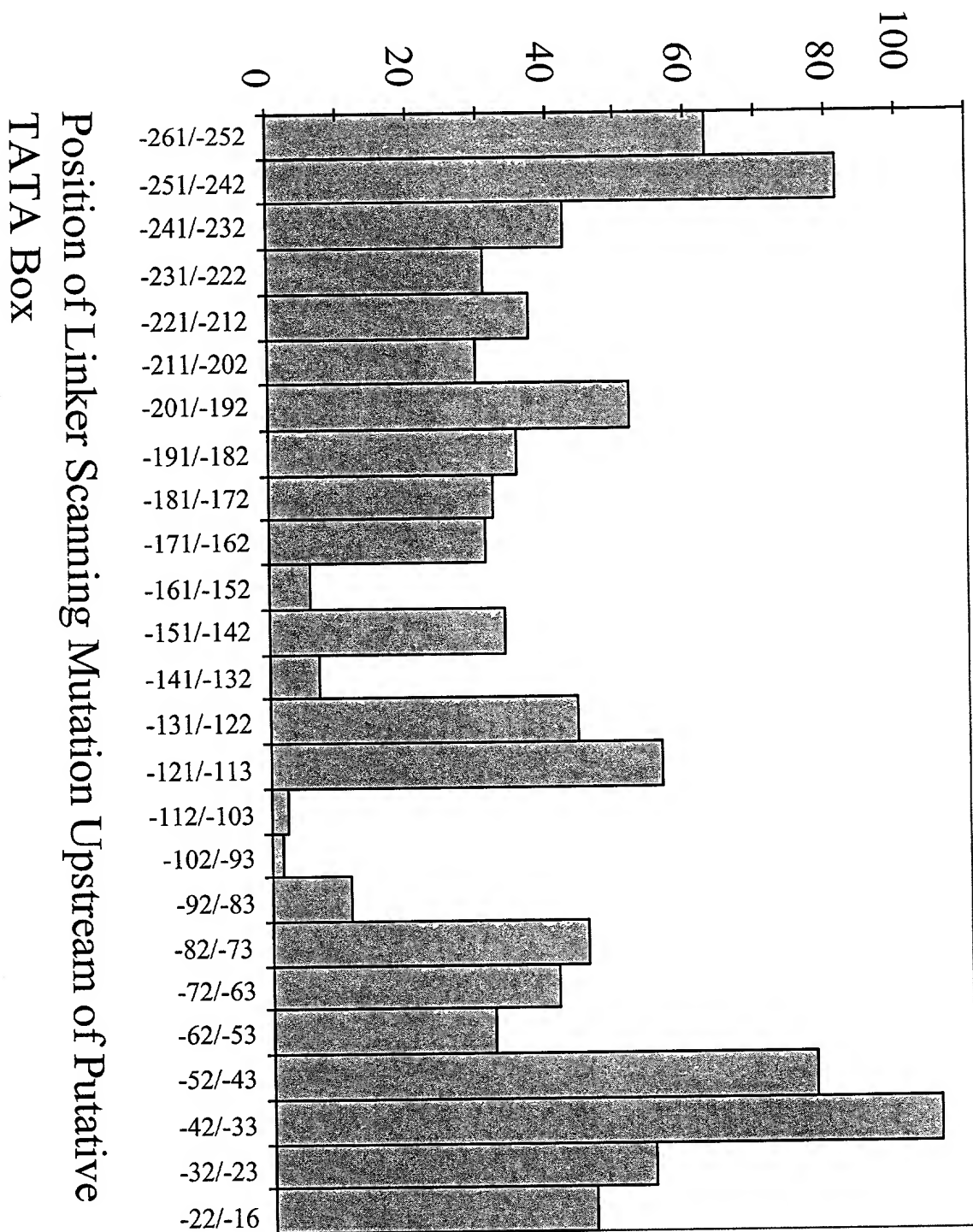


Figure 9

[illegible][illegible]

BS7	MS45	35S	PAT
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BS7:MS45

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9
10
11
12
13



Figure 11

